



#3

# SEQUENCE LISTING

<110> Shi, Jinrui  
Beach, Larry  
Wang, Hongyu  
Rafalski, Antoni J.  
Cahoon, Rebecca E.

<120> Novel Inositol Polyphosphate Kinase  
Genes and Uses Thereof

<130> 1286

<140> US 10/042,894

<141> 2002-01-09

<150> US 60/261,465

<151> 2001-01-12

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<221> CDS

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Met Pro Asp Leu His Pro Pro Glu His Gln  
1 5 10

gtc gcc ggt cac cgc gcc tcc gcc agc aag ctg gcc ccg ctc atc gac 161  
Val Ala Gly His Arg Ala Ser Ala Ser Lys Leu Gly Pro Leu Ile Asp  
15 20 25

ggc tcc gcc ctc ttc tac aag ccg ctc cag gcc gcc gac cgt ggg gag 209  
Gly Ser Gly Leu Phe Tyr Lys Pro Leu Gln Ala Gly Asp Arg Gly Glu  
30 35 40

cac gag gtc gcc ttc tat gag gcg ttc tcc gcc cac gcc gcc gtc ccg 257  
His Glu Val Ala Phe Tyr Glu Ala Phe Ser Ala His Ala Val Pro  
45 50 55

gcc cgc atc cga gac acc ttc ttc ccc ccg ttc cac gcc acg cga ctc 305  
Ala Arg Ile Arg Asp Thr Phe Phe Pro Arg Phe His Gly Thr Arg Leu  
60 65 70

ctc ccc acc gag gcg cag ccc ggg gag ccg cat ccg cac ctc gtc ctc 353

Leu	Pro	Thr	Glu	Ala	Gln	Pro	Gly	Glu	Pro	His	Pro	His	Leu	Val	Leu		
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gac	gac	ctc	ctc	gcg	ggg	ttt	gag	gcg	ccc	tgc	gtc	gca	gac	atc	aag	401	
Asp	Asp	Leu	Leu	Ala	Gly	Phe	Glu	Ala	Pro	Cys	Val	Ala	Asp	Ile	Lys		
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atc	ggc	gcc	atc	acg	tgg	cca	ccg	agt	tgc	ccg	gag	ccc	tac	atc	gcc	449	
Ile	Gly	Ala	Ile	Thr	Trp	Pro	Pro	Ser	Ser	Pro	Glu	Pro	Tyr	Ile	Ala		
			110					115					120				
aag	tac	ctc	gcc	aag	gac	cgc	ggg	acc	acg	agc	gtt	ctg	ctc	gga	ttc	497	
Lys	Tyr	Leu	Ala	Lys	Asp	Arg	Gly	Thr	Thr	Ser	Val	Leu	Leu	Gly	Phe		
			125				130						135				
cgc	gtc	ttg	cgt	ccg	agt	cgt	cgg	ccc	cga	ggg	cgc	cgt	gtg	gcg	gac	545	
Arg	Val	Leu	Arg	Pro	Ser	Arg	Arg	Pro	Arg	Gly	Arg	Val	Ala	Ala	Asp		
			140				145					150					
gga	gcg	ccc	gga	ggt	gaa	ggc	tat	gga	cac	cgt	cgg	cgt	ccg	ccg	cgt	593	
Gly	Ala	Pro	Gly	Gly	Glu	Gly	Tyr	Gly	His	Arg	Arg	Arg	Pro	Pro	Arg		
			155			160				165					170		
gct	ccg	gcg	cta	cgt	gtc	atc	cgc	ttg	ccg	acg	agg	gga	tgg	act	gcg	641	
Ala	Pro	Ala	Leu	Arg	Val	Ile	Arg	Leu	Pro	Thr	Arg	Gly	Trp	Thr	Ala		
				175					180					185			
cgc	tgc	cgg	cgg	cgg	tgt	acg	gag	gaa	aag	gtg	gag	tct	tgt	cac	agc	689	
Arg	Ser	Arg	Arg	Arg	Cys	Thr	Glu	Glu	Lys	Val	Glu	Ser	Cys	His	Ser		
				190					195					200			
tgc	gcg	agc	tca	agg	cat	ggt	tgg	agg	agc	aga	ctc	tgt	tcc	act	tct	737	
Cys	Ala	Ser	Ser	Arg	His	Gly	Trp	Arg	Ser	Arg	Leu	Cys	Ser	Thr	Ser		
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act	cgg	cgt	cga	ttc	ttc	tgg	gct	atg	atg	ctg	ctg	cag	tgc	cag	cag	785	
Thr	Arg	Arg	Arg	Phe	Phe	Trp	Ala	Met	Met	Leu	Leu	Gln	Ser	Gln	Gln		
			220			225						230					
gcg	gag	gtg	ggg	gtg	ggg	taa	cagtgaagct	ggtggacttt	gcccatgtgg							836	
Ala	Glu	Val	Gly	Val	Gly	*											
			235			240											
ccgagggtga	tgggggtgatt	gaccacaact	tcttgggcga	gctctgctag	ctgatcaagt	896											
tcgtttctga	cattgttcca	gagactcctt	agacgcagcc	tttggtcct	tcttaagaga	956											
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 Lys Pro Leu Gln Ala Gly Asp Arg Gly Glu His Glu Val Ala Phe Tyr  
 35 40 45  
 Glu Ala Phe Ser Ala His Ala Val Pro Ala Arg Ile Arg Asp Thr  
 50 55 60  
 Phe Phe Pro Arg Phe His Gly Thr Arg Leu Leu Pro Thr Glu Ala Gln  
 65 70 75 80  
 Pro Gly Glu Pro His Pro His Leu Val Leu Asp Asp Leu Leu Ala Gly  
 85 90 95  
 Phe Glu Ala Pro Cys Val Ala Asp Ile Lys Ile Gly Ala Ile Thr Trp  
 100 105 110  
 Pro Pro Ser Ser Pro Glu Pro Tyr Ile Ala Lys Tyr Leu Ala Lys Asp  
 115 120 125  
 Arg Gly Thr Thr Ser Val Leu Leu Gly Phe Arg Val Leu Arg Pro Ser  
 130 135 140  
 Arg Arg Pro Arg Gly Arg Val Ala Asp Gly Ala Pro Gly Gly Glu  
 145 150 155 160  
 Gly Tyr Gly His Arg Arg Arg Pro Pro Arg Ala Pro Ala Leu Arg Val  
 165 170 175  
 Ile Arg Leu Pro Thr Arg Gly Trp Thr Ala Arg Ser Arg Arg Cys  
 180 185 190  
 Thr Glu Glu Lys Val Glu Ser Cys His Ser Cys Ala Ser Ser Arg His  
 195 200 205  
 Gly Trp Arg Ser Arg Leu Cys Ser Thr Ser Thr Arg Arg Arg Phe Phe  
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 Trp Ala Met Met Leu Leu Gln Ser Gln Gln Ala Glu Val Gly Val Gly  
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<212> DNA

<213> Zea mays

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 Asp Leu His Pro Pro Glu His Gln Val Ala Gly His Arg Ala Ser Ala  
 5 10 15

agc aag ccg gcc ccg ctc atc gac gcc tcc gcc ctc ttc tac aag ccg 154  
 Ser Lys Pro Gly Pro Leu Ile Asp Gly Ser Gly Leu Phe Tyr Lys Pro  
 20 25 30

ctc cag gcc gcc gac cgt ggg gag cac gag gtc gct ttc tat gag gcg 202  
 Leu Gln Ala Gly Asp Arg Gly Glu His Glu Val Ala Phe Tyr Glu Ala

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Phe Ser Ala His Ala Val	Pro Ala Arg Ile Arg Asp Thr	Phe Phe		
55	60	65		
ccc cgg ttc cac gcc acg cga ctc ctc	ccc acc gag gcg cag ccc ggg	298		
Pro Arg Phe His Gly Thr Arg Leu Leu Pro Thr Glu Ala Gln Pro Gly				
70	75	80		
gag ccg cat ccg cac ctc gtc ctc gac gac ctc ctc gcg gga ttt gag	346			
Glu Pro His Pro His Leu Val Leu Asp Asp Leu Leu Ala Gly Phe Glu				
85	90	95		
gcg ccc tgc gtc gca gac atc aag atc gcc gcc atc acg tgg cca ccg	394			
Ala Pro Cys Val Ala Asp Ile Lys Ile Gly Ala Ile Thr Trp Pro Pro				
100	105	110		
agt tgc ccg gag ccc tac atc gcc aag tgc ctc gcc atg gac cgc ggg	442			
Ser Ser Pro Glu Pro Tyr Ile Ala Lys Cys Leu Ala Met Asp Arg Gly				
115	120	125	130	
acc acg agc gtt ctg ctc gga ttc cgc gtc tcc gcc gtc cga gtc gtc	490			
Thr Thr Ser Val Leu Leu Gly Phe Arg Val Ser Gly Val Arg Val Val				
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gtc ccc gag gcc gcc gtg tgg ccg acg gag cgc ccg gag gtg aag gct	538			
Val Pro Glu Gly Ala Val Trp Arg Thr Glu Arg Pro Glu Val Lys Ala				
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Met Asp Thr Val Gly Val Arg Arg Val Leu Arg Arg Tyr Val Ser Ser				
165	170	175		
gct tgc cga cga ggg gat gga ctg cgc gct cgc gcc gcc ggt gta ccg	634			
Ala Cys Arg Arg Gly Asp Gly Leu Arg Ala Arg Gly Gly Gly Val Arg				
180	185	190		
agg aaa agg tgg agt ctt gtc act gct gcg cga gct caa gcc gtg gtt	682			
Arg Lys Arg Trp Ser Leu Val Thr Ala Ala Arg Ala Gln Gly Val Val				
195	200	205	210	
cga gga gca gcc tct gtt cca ctt cta ctc gcc gtc gat tct tct ggg	730			
Arg Gly Ala Ala Ser Val Pro Leu Leu Leu Gly Val Asp Ser Ser Gly				
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cta tga tgctgctgca gtcgcagcag gccgaggtgg ggggtgggta acagtgaagc	786			
Leu *				
tggtggactt tgcccattgtg gccgaggggtg atgggggtgat tgaccacaac ttcctgggag	846			
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Lys Pro Leu Gln Ala Gly Asp Arg Gly Glu His Glu Val Ala Phe Tyr  
35 40 45  
Glu Ala Phe Ser Ala His Ala Val Pro Ala Arg Ile Arg Asp Thr  
50 55 60  
Phe Phe Pro Arg Phe His Gly Thr Arg Leu Leu Pro Thr Glu Ala Gln  
65 70 75 80  
Pro Gly Glu Pro His Pro His Leu Val Leu Asp Asp Leu Leu Ala Gly  
85 90 95  
Phe Glu Ala Pro Cys Val Ala Asp Ile Lys Ile Gly Ala Ile Thr Trp  
100 105 110  
Pro Pro Ser Ser Pro Glu Pro Tyr Ile Ala Lys Cys Leu Ala Met Asp  
115 120 125  
Arg Gly Thr Thr Ser Val Leu Leu Gly Phe Arg Val Ser Gly Val Arg  
130 135 140  
Val Val Val Pro Glu Gly Ala Val Trp Arg Thr Glu Arg Pro Glu Val  
145 150 155 160  
Lys Ala Met Asp Thr Val Gly Val Arg Arg Val Leu Arg Arg Tyr Val  
165 170 175  
Ser Ser Ala Cys Arg Arg Gly Asp Gly Leu Arg Ala Arg Gly Gly Gly  
180 185 190  
Val Arg Arg Lys Arg Trp Ser Leu Val Thr Ala Ala Arg Ala Gln Gly  
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Ser Gly Leu  
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Asp Leu His Pro Pro Glu His Gln Val Ala Gly His Arg Ala Ser Ala  
5 10 15  
agc aag ccg ggc ccg ctc atc gac ggc tcc ggc ctc ttc tac aag ccg 154  
Ser Lys Pro Gly Pro Leu Ile Asp Gly Ser Gly Leu Phe Tyr Lys Pro

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gag ccg cat ccg cac ctc gtc ctc gac gac ctc ctc gcg gga ttt gag 346 Glu Pro His Pro His Leu Val Leu Asp Asp Leu Leu Ala Gly Phe Glu 85 90 95			
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ggc ccc gag gcc gcc gtg tgg ccg acg gag cgc ccg gag gtg aag gcc 538 Gly Pro Glu Gly Ala Val Trp Arg Thr Glu Arg Pro Glu Val Lys Ala 150 155 160			
atg gac acc gcc gcc gtc cgc cgc gtg ctc ccg cgc tac gtg tca tcc 586 Met Asp Thr Ala Gly Val Arg Arg Val Leu Arg Arg Tyr Val Ser Ser 165 170 175			
gtt gcc gac gag ggg atg gac tgt gcg ctc gcc gcg gcg gtg tac gga 634 Val Ala Asp Glu Gly Met Asp Cys Ala Leu Ala Ala Ala Val Tyr Gly 180 185 190			
gga aaa ggt gga gtc ttg tca cag ctg cgc gag ctc aag gcg tgg ttc 682 Gly Lys Gly Gly Val Leu Ser Gln Leu Arg Glu Leu Lys Ala Trp Phe 195 200 205 210			
gag gag cag act ctg ttc cac ttc tac tcc gcg tcc att ctt ctg gcc 730 Glu Glu Gln Thr Leu Phe His Phe Tyr Ser Ala Ser Ile Leu Leu Gly 215 220 225			
tat gat gct gct gca gtc gca gca gcc gga ggt ggg ggt ggg gtg acg 778 Tyr Asp Ala Ala Ala Val Ala Ala Gly Gly Gly Gly Gly Val Thr 230 235 240			
gtg aag ctg gtg gac ttt gcc cat gtg gcc gag ggt gat ggg gtg att 826 Val Lys Leu Val Asp Phe Ala His Val Ala Glu Gly Asp Gly Val Ile			

245 250 255

gac cac aac ttc ctg ggc ggg ctc tgc tgc ctg atc aag ttc gtt tct 874  
 Asp His Asn Phe Leu Gly Gly Leu Cys Ser Leu Ile Lys Phe Val Ser  
 260 265 270

gac att gtt cca gag act cct cag acg cag cct ttg ggt cct tct taa 922  
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g 923

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 Lys Pro Leu Gln Ala Gly Asp Arg Gly Glu His Glu Val Ala Phe Tyr  
 35 40 45  
 Glu Ala Phe Ser Ala His Ala Ala Val Pro Ala Arg Ile Arg Asp Thr  
 50 55 60  
 Phe Phe Pro Arg Phe His Gly Thr Arg Leu Leu Pro Thr Glu Ala Gln  
 65 70 75 80  
 Pro Gly Glu Pro His Pro His Leu Val Leu Asp Asp Leu Leu Ala Gly  
 85 90 95  
 Phe Glu Ala Pro Cys Val Ala Asp Ile Lys Ile Gly Ala Ile Thr Trp  
 100 105 110  
 Pro Pro Ser Ser Pro Glu Pro Tyr Ile Ala Lys Cys Leu Ala Met Asp  
 115 120 125  
 Arg Gly Thr Thr Ser Val Leu Leu Gly Phe Arg Val Ser Gly Val Arg  
 130 135 140  
 Val Val Gly Pro Glu Gly Ala Val Trp Arg Thr Glu Arg Pro Glu Val  
 145 150 155 160  
 Lys Ala Met Asp Thr Ala Gly Val Arg Arg Val Leu Arg Arg Tyr Val  
 165 170 175  
 Ser Ser Val Ala Asp Glu Gly Met Asp Cys Ala Leu Ala Ala Val  
 180 185 190  
 Tyr Gly Gly Lys Gly Gly Val Leu Ser Gln Leu Arg Glu Leu Lys Ala  
 195 200 205  
 Trp Phe Glu Glu Gln Thr Leu Phe His Phe Tyr Ser Ala Ser Ile Leu  
 210 215 220  
 Leu Gly Tyr Asp Ala Ala Ala Val Ala Ala Gly Gly Gly Gly Gly  
 225 230 235 240  
 Val Thr Val Lys Leu Val Asp Phe Ala His Val Ala Glu Gly Asp Gly  
 245 250 255  
 Val Ile Asp His Asn Phe Leu Gly Gly Leu Cys Ser Leu Ile Lys Phe  
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 Ser Lys Leu Gly Pro Leu Ile Asp Gly Ser Gly Leu Phe Tyr Lys Pro  
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 Leu Gln Ala Gly Asp Arg Gly Glu His Val Ala Phe Tyr Glu Ala  
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ccc cgg ttc cac ggc acg cga ctc ctc ccc acc gag cgc cag ccc ggg 297  
 Pro Arg Phe His Gly Thr Arg Leu Leu Pro Thr Glu Ala Gln Pro Gly  
 70 75 80

gag ccg cat cct cac ctc gtc ctc gac gac ctc ctc cgc ggg ttt cag 345  
 Glu Pro His Pro His Leu Val Leu Asp Asp Leu Leu Ala Gly Phe Gln  
 85 90 95

gcg ccc tgc gtc gca gac atc aag atc ggc gcc atc acg tgg cca ccg 393  
 Ala Pro Cys Val Ala Asp Ile Lys Ile Gly Ala Ile Thr Trp Pro Pro  
 100 105 110

agt tgc ccg gag ccc tac atc gcc aag tgc ctc gcc aag gac cgc ggg 441  
 Ser Ser Pro Glu Pro Tyr Ile Ala Lys Cys Leu Ala Lys Asp Arg Gly  
 115 120 125 130

acc acg agc gtt ctg ctc gga ttc cgc gtc tcc ggc gtc cga gtc gtc 489  
 Thr Thr Ser Val Leu Leu Gly Phe Arg Val Ser Gly Val Arg Val Val  
 135 140 145

ggc ccc gag ggc gcc gtg tgg cgg acg gag cgc ccg gag gtg aag gcc 537  
 Gly Pro Glu Gly Ala Val Trp Arg Thr Glu Arg Pro Glu Val Lys Ala  
 150 155 160



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 Met Asp Thr Ala Gly Val Arg Arg Val Leu Arg Arg Tyr Val Ser Ser  
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gtt gcc gac gag ggg atg gac tgt gcg ctc gcc gcg gcg gtg tac gga 633  
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gga aaa ggt gga gtc ttg tca cag ctg cgc gag ctc aag gcg tgg ttc 681  
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 215 220 225

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 Tyr Asp Ala Ala Val Ala Ala Gly Gly Asp Gly Gly Val Thr  
 230 235 240

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 Val Lys Leu Val Asp Phe Ala His Val Ala Glu Gly Asp Gly Val Ile  
 245 250 255

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 Asp His Asn Phe Leu Gly Gly Leu Cys Ser Leu Ile Lys Phe Val Ser  
 260 265 270

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 Asp Ile Val Pro Glu Thr Pro His Thr Gln Pro Leu Gly Pro Ser \*  
 275 280 285

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 35 40 45  
 Glu Ala Phe Ser Ala His Ala Ala Val Pro Ala Arg Ile Arg Asp Thr  
 50 55 60  
 Phe Phe Pro Arg Phe His Gly Thr Arg Leu Leu Pro Thr Glu Ala Gln

65					70					75				80
Pro	Gly	Glu	Pro	His	Pro	His	Leu	Val	Leu	Asp	Asp	Leu	Leu	Ala Gly
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Phe	Gln	Ala	Pro	Cys	Val	Ala	Asp	Ile	Lys	Ile	Gly	Ala	Ile	Thr Trp
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Pro	Pro	Ser	Ser	Pro	Glu	Pro	Tyr	Ile	Ala	Lys	Cys	Leu	Ala	Lys Asp
		115					120						125	
Arg	Gly	Thr	Thr	Ser	Val	Leu	Leu	Gly	Phe	Arg	Val	Ser	Gly	Val Arg
		130				135					140			
Val	Val	Gly	Pro	Glu	Gly	Ala	Val	Trp	Arg	Thr	Glu	Arg	Pro	Glu Val
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Lys	Ala	Met	Asp	Thr	Ala	Gly	Val	Arg	Arg	Val	Leu	Arg	Arg	Tyr Val
			165					170					175	
Ser	Ser	Val	Ala	Asp	Glu	Gly	Met	Asp	Cys	Ala	Leu	Ala	Ala	Ala Val
		180						185					190	
Tyr	Gly	Gly	Lys	Gly	Gly	Val	Leu	Ser	Gln	Leu	Arg	Glu	Leu	Lys Ala
		195					200					205		
Trp	Phe	Glu	Glu	Gln	Thr	Leu	Phe	His	Phe	Tyr	Ser	Ala	Ser	Ile Leu
		210				215					220			
Leu	Gly	Tyr	Asp	Ala	Ala	Ala	Val	Ala	Ala	Gly	Gly	Asp	Gly	Gly Gly
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Val	Thr	Val	Lys	Leu	Val	Asp	Phe	Ala	His	Val	Ala	Glu	Gly	Asp Gly
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1

5

10

gcc aag gac gga atc ctg ggc cca ctc gtc gac gat ttt gga aaa ttc 98

Ala Lys Asp Gly Ile Leu Gly Pro Leu Val Asp Asp Phe Gly Lys Phe

15

20

25

tac aag ccc ctc cag acc aac aaa gac gac gac acc cgc ggc tcc acc 146

Tyr Lys Pro Leu Gln Thr Asn Lys Asp Asp Thr Arg Gly Ser Thr

30

35

40

45

gaa ctc tcc ttt tac acc tct ctc gcc gcc gcc cac gac tac tcc 194

Glu Leu Ser Phe Tyr Thr Ser Leu Ala Ala Ala His Asp Tyr Ser

50

55

60

atc cgc tcc ttc ttc ccc gcc ttt cac ggc acc cgc ctc ctg gac gcc	242
Ile Arg Ser Phe Phe Pro Ala Phe His Gly Thr Arg Leu Asp Ala	
65 70 75	
tcc gac ggc tcc ggt ccc cac cct cac ctg gtc ctg gag gac ctc ctc	290
Ser Asp Gly Ser Gly Pro His Pro His Leu Val Leu Glu Asp Leu Leu	
80 85 90	
tgc ggc tac tcc aaa ccc tcc gtc atg gac gta aag atc ggc tcc aga	338
Cys Gly Tyr Ser Lys Pro Ser Val Met Asp Val Lys Ile Gly Ser Arg	
95 100 105	
acc tgg cac ctg gga gac tcc gag gac tac atc tgc aag tgc ctg aag	386
Thr Trp His Leu Gly Asp Ser Glu Asp Tyr Ile Cys Lys Cys Leu Lys	
110 115 120 125	
aag gac aga gag tcc tct agc ttg ccc ttg ggt ttc aga atc tgc gga	434
Lys Asp Arg Glu Ser Ser Leu Pro Leu Gly Phe Arg Ile Ser Gly	
130 135 140	
gtc aag gac tct atc tcc tcc tgg gaa cct acc agg aaa tct ctc cag	482
Val Lys Asp Ser Ile Ser Ser Trp Glu Pro Thr Arg Lys Ser Leu Gln	
145 150 155	
tgt cta tcc gcc cat ggt gtt gca ctt gtt ctc aac aag ttc gtt tcc	530
Cys Leu Ser Ala His Gly Val Ala Leu Val Leu Asn Lys Phe Val Ser	
160 165 170	
tct aat aat atc aac cat gat gat cat cat ccc gat tgc gct ttc gca	578
Ser Asn Asn Ile Asn His Asp Asp His His Pro Asp Cys Ala Phe Ala	
175 180 185	
acg gag gtc tac ggc gcc gtt ttg gag cgc ttg cag aag ctc aag gac	626
Thr Glu Val Tyr Gly Ala Val Leu Glu Arg Leu Gln Lys Leu Lys Asp	
190 195 200 205	
tgg ttc gag gtt cag acg gtg tat cac ttc tat tct tgt tct gtt ctt	674
Trp Phe Glu Val Gln Thr Val Tyr His Phe Tyr Ser Cys Ser Val Leu	
210 215 220	
gtg gtg tac gag aag gat cta ggg aaa ggg aaa gct acc aac cct ctg	722
Val Val Tyr Glu Lys Asp Leu Gly Lys Gly Lys Ala Thr Asn Pro Leu	
225 230 235	
gtc aaa ctc gtt gac ttt gca cac gtg gtg gac gga aac ggt gtc att	770
Val Lys Leu Val Asp Phe Ala His Val Val Asp Gly Asn Gly Val Ile	
240 245 250	
gat cac aac ttc ttg ggt ggc ctt tgt tcc ttc atc aag ttc ctc aag	818
Asp His Asn Phe Leu Gly Gly Leu Cys Ser Phe Ile Lys Phe Leu Lys	
255 260 265	
gat atc cta gca gta gca tgt ctt cac aag tga ctgattttca tcgagttaat	871
Asp Ile Leu Ala Val Ala Cys Leu His Lys *	
270 275	

cttattccta tcagaaaaata attatgcttg aattagtgtc gcagactaac tgtttgaagt 931  
 actgtcagaa acaaaaataat aatattggact gagaggcaat ctgtttctgc taaactccct 991  
 ttcaagttgc tgtcagatac tagcgtgcc ttttctttt tcatattctg tcaaaagtga 1051  
 tcatttaata ataataacaa tgtccttcaa ctccaaaaaa aaaaaaaaaa aaaa 1105

<210> 10

<211> 279

<212> PRT

<213> Glycine max

<400> 10

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 Gly Ile Leu Gly Pro Leu Val Asp Asp Phe Gly Lys Phe Tyr Lys Pro  
 20 25 30  
 Leu Gln Thr Asn Lys Asp Asp Thr Arg Gly Ser Thr Glu Leu Ser  
 35 40 45  
 Phe Tyr Thr Ser Leu Ala Ala Ala His Asp Tyr Ser Ile Arg Ser  
 50 55 60  
 Phe Phe Pro Ala Phe His Gly Thr Arg Leu Leu Asp Ala Ser Asp Gly  
 65 70 75 80  
 Ser Gly Pro His Pro His Leu Val Leu Glu Asp Leu Leu Cys Gly Tyr  
 85 90 95  
 Ser Lys Pro Ser Val Met Asp Val Lys Ile Gly Ser Arg Thr Trp His  
 100 105 110  
 Leu Gly Asp Ser Glu Asp Tyr Ile Cys Lys Cys Leu Lys Lys Asp Arg  
 115 120 125  
 Glu Ser Ser Ser Leu Pro Leu Gly Phe Arg Ile Ser Gly Val Lys Asp  
 130 135 140  
 Ser Ile Ser Ser Trp Glu Pro Thr Arg Lys Ser Leu Gln Cys Leu Ser  
 145 150 155 160  
 Ala His Gly Val Ala Leu Val Leu Asn Lys Phe Val Ser Ser Asn Asn  
 165 170 175  
 Ile Asn His Asp Asp His His Pro Asp Cys Ala Phe Ala Thr Glu Val  
 180 185 190  
 Tyr Gly Ala Val Leu Glu Arg Leu Gln Lys Leu Lys Asp Trp Phe Glu  
 195 200 205  
 Val Gln Thr Val Tyr His Phe Tyr Ser Cys Ser Val Leu Val Val Tyr  
 210 215 220  
 Glu Lys Asp Leu Gly Lys Gly Lys Ala Thr Asn Pro Leu Val Lys Leu  
 225 230 235 240  
 Val Asp Phe Ala His Val Val Asp Gly Asn Gly Val Ile Asp His Asn  
 245 250 255  
 Phe Leu Gly Gly Leu Cys Ser Phe Ile Lys Phe Leu Lys Asp Ile Leu  
 260 265 270  
 Ala Val Ala Cys Leu His Lys  
 275

<210> 11

<211> 1195

<212> DNA

<213> Eucalyptus grandis

<220>

<221> CDS

<222> (116)...(1048)

<400> 11

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gcaccagctt cttggagtag ttgccatca gcgtaggattt tcattttagt ccattctggct 60
gtgatcaatc gaattctgagt aagtttggag aattttttcgc cacatcagat acacc atg 118
                                         Met
                                         1

ctc aag gtc cgc gat cat caa gtc gcc ggt cac cgg gga gac ggg gga 166
Leu Lys Val Pro Asp His Gln Val Ala Gly His Arg Gly Asp Gly Gly
                    5                    10                    15

aag ctg ggg cca ctg gtg gat gat tcg ggc cgc ttc tat aag cct ctc 214
Lys Leu Gly Pro Leu Val Asp Asp Ser Gly Arg Phe Tyr Lys Pro Leu
                    20                    25                    30

cag agc gat cat cgc gga gac acg gaa gtg gcc ttt tac gag tca ttc 262
Gln Ser Asp His Arg Gly Asp Thr Glu Val Ala Phe Tyr Glu Ser Phe
                    35                    40                    45

tat tcc aat acc gag atc cca ggt cac att cgc aaa ttc ttt cct gcg 310
Tyr Ser Asn Thr Glu Ile Pro Gly His Ile Arg Lys Phe Phe Pro Ala
                    50                    55                    60                    65

ttt cac gga act aag act att gag cgc tct gat gga tcg ggt cct caa 358
Phe His Gly Thr Lys Thr Ile Glu Ala Ser Asp Gly Ser Gly Pro Gln
                    70                    75                    80

cct cac ctg gtt ctg gag gat ctc gtc tcg ggt cgc acg aac cca tct 406
Pro His Leu Val Leu Glu Asp Leu Val Ser Gly Arg Thr Asn Pro Ser
                    85                    90                    95

ctc atg gac atc aag act gga tcc aga aca tgg tat cgc gag gcc tct 454
Leu Met Asp Ile Lys Thr Gly Ser Arg Thr Trp Tyr Pro Glu Ala Ser
                    100                    105                    110

gag gag tac atc caa aag tgc tta gag aaa gat cga aat agc aca agc 502
Glu Glu Tyr Ile Gln Lys Cys Leu Glu Lys Asp Arg Asn Ser Thr Ser
                    115                    120                    125

gtt tca ttg ggt ttt agg att tct ggg cta agg gta tat caa aat agc 550
Val Ser Leu Gly Phe Arg Ile Ser Gly Leu Arg Val Tyr Gln Asn Ser
                    130                    135                    140                    145

gaa gct gga ttt tgg caa cct gag aag aag gtt gtt tat agc ttt aat 598
Glu Ala Gly Phe Trp Gln Pro Glu, Lys Lys Val Val Tyr Ser Phe Asn
                    150                    155                    160

gcg gac ggt gtc agg tcg gct ctg agg aag ttt gtt tct tcc aac ttg 646
Ala Asp Gly Val Arg Ser Ala Leu Arg Lys Phe Val Ser Ser Asn Leu
                    165                    170                    175

tct ctg ggt cca aat gtg gat ccg gat tgt ttg tat gca tca aaa gtt 694
Ser Leu Gly Pro Asn Val Asp Pro Asp Cys Leu Tyr Ala Ser Lys Val
                    180                    185                    190
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tac tgt cac cgg ggt gga att ttg gca caa ttg ctt cag ctg aag gaa 742  
 Tyr Cys His Arg Gly Gly Ile Leu Ala Gln Leu Leu Gln Leu Lys Glu  
 195 200 205

tgg ttt gag gtt cag acg aat tat cac ttc tat tct tgt tca ctc att 790  
 Trp Phe Glu Val Gln Thr Asn Tyr His Phe Tyr Ser Cys Ser Leu Ile  
 210 215 220 225

atc tta tat gac agg gag tct gct ttg gac ggc tgt gca cac ccg aaa 838  
 Ile Leu Tyr Asp Arg Glu Ser Ala Leu Asp Gly Cys Ala His Pro Lys  
 230 235 240

gtt aaa ctg gtg gac ttt gca cat gtg atg gat ggc cac ggc gtg atc 886  
 Val Lys Leu Val Asp Phe Ala His Val Met Asp Gly His Gly Val Ile  
 245 250 255

gat cac aac ttc ttg ggt ggc ctc tgt tct gta atc aag ttt ata cgt 934  
 Asp His Asn Phe Leu Gly Gly Leu Cys Ser Val Ile Lys Phe Ile Arg  
 260 265 270

gac att gct gat gaa gat aac aag tgt gca aag tgc gaa gtc aat ctt 982  
 Asp Ile Ala Asp Glu Asp Asn Lys Cys Ala Lys Cys Glu Val Asn Leu  
 275 280 285

gga ttg aaa gaa aat ggc ttc tat aag agc agc acg gaa cca gag ctt 1030  
 Gly Leu Lys Glu Asn Gly Phe Tyr Lys Ser Ser Thr Glu Pro Glu Leu  
 290 295 300 305

gat cac gag gcc tgc tag tggaactgg agaataactg cattcatgca 1078  
 Asp His Glu Ala Cys \*  
 310

ttctgcatt cctgctctga caagtgggtc agaatgggta taataacagt ctatttttagt 1138  
 caaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa 1195

<210> 12  
 <211> 310  
 <212> PRT  
 <213> Eucalyptus grandis

<400> 12  
 Met Leu Lys Val Pro Asp His Gln Val Ala Gly His Arg Gly Asp Gly  
 1 5 10 15  
 Gly Lys Leu Gly Pro Leu Val Asp Asp Ser Gly Arg Phe Tyr Lys Pro  
 20 25 30  
 Leu Gln Ser Asp His Arg Gly Asp Thr Glu Val Ala Phe Tyr Glu Ser  
 35 40 45  
 Phe Tyr Ser Asn Thr Glu Ile Pro Gly His Ile Arg Lys Phe Phe Pro  
 50 55 60  
 Ala Phe His Gly Thr Lys Thr Ile Glu Ala Ser Asp Gly Ser Gly Pro  
 65 70 75 80  
 Gln Pro His Leu Val Leu Glu Asp Leu Val Ser Gly Arg Thr Asn Pro  
 85 90 95  
 Ser Leu Met Asp Ile Lys Thr Gly Ser Arg Thr Trp Tyr Pro Glu Ala  
 100 105 110

Ser Glu Glu Tyr Ile Gln Lys Cys Leu Glu Lys Asp Arg Asn Ser Thr  
115 120 125  
Ser Val Ser Leu Gly Phe Arg Ile Ser Gly Leu Arg Val Tyr Gln Asn  
130 135 140  
Ser Glu Ala Gly Phe Trp Gln Pro Glu Lys Lys Val Val Tyr Ser Phe  
145 150 155 160  
Asn Ala Asp Gly Val Arg Ser Ala Leu Arg Lys Phe Val Ser Ser Asn  
165 170 175  
Leu Ser Leu Gly Pro Asn Val Asp Pro Asp Cys Leu Tyr Ala Ser Lys  
180 185 190  
Val Tyr Cys His Arg Gly Gly Ile Leu Ala Gln Leu Leu Gln Leu Lys  
195 200 205  
Glu Trp Phe Glu Val Gln Thr Asn Tyr His Phe Tyr Ser Cys Ser Leu  
210 215 220  
Ile Ile Leu Tyr Asp Arg Glu Ser Ala Leu Asp Gly Cys Ala His Pro  
225 230 235 240  
Lys Val Lys Leu Val Asp Phe Ala His Val Met Asp Gly His Gly Val  
245 250 255  
Ile Asp His Asn Phe Leu Gly Gly Leu Cys Ser Val Ile Lys Phe Ile  
260 265 270  
Arg Asp Ile Ala Asp Glu Asp Asn Lys Cys Ala Lys Cys Glu Val Asn  
275 280 285  
Leu Gly Leu Lys Glu Asn Gly Phe Tyr Lys Ser Ser Thr Glu Pro Glu  
290 295 300  
Leu Asp His Glu Ala Cys  
305 310

<210> 13

<211> 1020

<212> DNA

<213> Parthenium argentatum

<220>

<221> CDS

<222> (21)...(908)

<400> 13

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Met Leu Lys Ala Pro Asp His Gln Val Ala Gly  
1 5 10

cat gaa gct ggg ctc ggg aag ctt ggc cca ctc att gat gat tca ggc 101  
His Glu Ala Gly Leu Gly Lys Leu Gly Pro Leu Ile Asp Asp Ser Gly  
15 20 25

cgg ttt tac aaa cca ctg cag ggt gat aac cgt ggg tca gaa gaa gta 149  
Arg Phe Tyr Lys Pro Leu Gln Gly Asp Asn Arg Gly Ser Glu Glu Val  
30 35 40

gcc ttt tat gaa tca ttt tct tct aac aat aat att cca gaa cac ata 197  
Ala Phe Tyr Glu Ser Phe Ser Ser Asn Asn Asn Ile Pro Glu His Ile  
45 50 55

cgc aaa ttc ttt cct ata tat tat ggc acc aaa atc atg aag gca tcc 245  
Arg Lys Phe Phe Pro Ile Tyr Tyr Gly Thr Lys Ile Met Lys Ala Ser

60	65							70				75				
act ggc tct gac cat cct cac atg gtg ttg caa gat ctt aca tca gct	Thr Gly Ser Asp His Pro His Met Val Leu Gln Asp Leu Thr Ser Ala	293														
	80						85						90			
cat gtc aac cca tct gta atg gac atc aaa atc ggg tcc aga aca tgg	His Val Asn Pro Ser Val Met Asp Ile Lys Ile Gly Ser Arg Thr Trp	341														
	95						100						105			
gcg cca gaa gct tcc gag gcg tac att gca aaa tgc tta aaa aag gat	Ala Pro Glu Ala Ser Glu Ala Tyr Ile Ala Lys Cys Leu Lys Lys Asp	389														
	110					115					120					
agg gaa agc aca agt att cca ttg gga ttc agg atc tcc ggg ctg caa	Arg Glu Ser Thr Ser Ile Pro Leu Gly Phe Arg Ile Ser Gly Leu Gln	437														
	125				130					135						
gtc tat atc gat gat ggg tca ggg ttt tat aag cct cat aga aat tac	Val Tyr Ile Asp Asp Gly Ser Gly Phe Tyr Lys Pro His Arg Asn Tyr	485														
	140			145				150						155		
atg cgt aaa acc ggc cca gct gat gtt aga cta ctt ctt agg aaa ttt	Met Arg Lys Thr Gly Pro Ala Asp Val Arg Leu Leu Leu Arg Lys Phe	533														
			160				165						170			
gtt tct tct aac ccg tct gca gag atg gaa atg cgc aca ggc cta ggc	Val Ser Ser Asn Pro Ser Ala Glu Met Glu Met Arg Thr Gly Leu Gly	581														
			175				180					185				
ccg gat tgt tct tta gca tct ttt gtt tat ggt ggg cct aat ggg ata	Pro Asp Cys Ser Leu Ala Ser Phe Val Tyr Gly Gly Pro Asn Gly Ile	629														
			190			195					200					
tta gct caa ctg atg gaa ttg aag aca tgg ttt gaa gat caa aca att	Leu Ala Gln Leu Met Glu Leu Lys Thr Trp Phe Glu Asp Gln Thr Ile	677														
			205		210					215						
tac cac ttc tat gct tgt tct ttt ttg ttc atc ttt gaa aag agg ttg	Tyr His Phe Tyr Ala Cys Ser Phe Leu Phe Ile Phe Glu Lys Arg Leu	725														
	220			225					230				235			
gtg tta aaa ggt gct cgg tca aac gca gaa gtc aaa ctt att gat ttt	Val Leu Lys Gly Ala Arg Ser Asn Ala Glu Val Lys Leu Ile Asp Phe	773														
			240				245					250				
gct cat gtt aca gat ggt aat ggt gtt att gat cac aat ttc ttg ggt	Ala His Val Thr Asp Gly Asn Gly Val Ile Asp His Asn Phe Leu Gly	821														
			255				260					265				
ggg ctg tgt tct ttg ata aag ttc att tct gac ata ctt tcg gag aca	Gly Leu Cys Ser Leu Ile Lys Phe Ile Ser Asp Ile Leu Ser Glu Thr	869														
			270			275					280					
aaa gat tgt aat ggt aca aac ggt cag gtt gaa ctt tga aactctcttc	Lys Asp Cys Asn Gly Thr Asn Gly Gln Val Glu Leu *	918														



285

290

295

ttgttgcttt tcttcaataa tttatcatga cagtgtttta ttgttaaagat attcgcttac 978  
 cggaatatat cttgtggtatg agtgaaaaaa aaaaaaaaaa aa 1020

&lt;210&gt; 14

&lt;211&gt; 295

&lt;212&gt; PRT

&lt;213&gt; Parthenium argentatum

&lt;400&gt; 14

Met Leu Lys Ala Pro Asp His Gln Val Ala Gly His Glu Ala Gly Leu  
 1 5 10 15  
 Gly Lys Leu Gly Pro Leu Ile Asp Asp Ser Gly Arg Phe Tyr Lys Pro  
 20 25 30  
 Leu Gln Gly Asp Asn Arg Gly Ser Glu Glu Val Ala Phe Tyr Glu Ser  
 35 40 45  
 Phe Ser Ser Asn Asn Asn Ile Pro Glu His Ile Arg Lys Phe Phe Pro  
 50 55 60  
 Ile Tyr Tyr Gly Thr Lys Ile Met Lys Ala Ser Thr Gly Ser Asp His  
 65 70 75 80  
 Pro His Met Val Leu Gln Asp Leu Thr Ser Ala His Val Asn Pro Ser  
 85 90 95  
 Val Met Asp Ile Lys Ile Gly Ser Arg Thr Trp Ala Pro Glu Ala Ser  
 100 105 110  
 Glu Ala Tyr Ile Ala Lys Cys Leu Lys Lys Asp Arg Glu Ser Thr Ser  
 115 120 125  
 Ile Pro Leu Gly Phe Arg Ile Ser Gly Leu Gln Val Tyr Ile Asp Asp  
 130 135 140  
 Gly Ser Gly Phe Tyr Lys Pro His Arg Asn Tyr Met Arg Lys Thr Gly  
 145 150 155 160  
 Pro Ala Asp Val Arg Leu Leu Leu Arg Lys Phe Val Ser Ser Asn Pro  
 165 170 175  
 Ser Ala Glu Met Glu Met Arg Thr Gly Leu Gly Pro Asp Cys Ser Leu  
 180 185 190  
 Ala Ser Phe Val Tyr Gly Gly Pro Asn Gly Ile Leu Ala Gln Leu Met  
 195 200 205  
 Glu Leu Lys Thr Trp Phe Glu Asp Gln Thr Ile Tyr His Phe Tyr Ala  
 210 215 220  
 Cys Ser Phe Leu Phe Ile Phe Glu Lys Arg Leu Val Leu Lys Gly Ala  
 225 230 235 240  
 Arg Ser Asn Ala Glu Val Lys Leu Ile Asp Phe Ala His Val Thr Asp  
 245 250 255  
 Gly Asn Gly Val Ile Asp His Asn Phe Leu Gly Gly Leu Cys Ser Leu  
 260 265 270  
 Ile Lys Phe Ile Ser Asp Ile Leu Ser Glu Thr Lys Asp Cys Asn Gly  
 275 280 285  
 Thr Asn Gly Gln Val Glu Leu  
 290 295

&lt;210&gt; 15

&lt;211&gt; 899

&lt;212&gt; DNA

&lt;213&gt; Zea mays

<220>  
 <221> CDS  
 <222> (89) ... (424)

<400> 15  
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 cacccttgc tcccatagtc cccatacc atg ccc gac ctc cac ccg ccg gag 112  
 Met Pro Asp Leu His Pro Pro Glu  
 1 5  
 cac caa gtc gcc ggt cac cgc gcc tcc gcc agc aag ctg ggc cca ctc 160  
 His Gln Val Ala Gly His Arg Ala Ser Ala Ser Lys Leu Gly Pro Leu  
 10 15 20  
 atc gac ggc tct ggc ctc ttc tac aag ccg ctc cag gcc ggc gac cgt 208  
 Ile Asp Gly Ser Gly Leu Phe Tyr Lys Pro Leu Gln Ala Gly Asp Arg  
 25 30 35 40  
 ggg gag cac gag gtc gcc ttc tat gag gcg ttc tcc gcc cac gcc gcc 256  
 Gly Glu His Glu Val Ala Phe Tyr Glu Ala Phe Ser Ala His Ala Ala  
 45 50 55  
 gtc ccg gcc cgc atc cga gac acc ttc ttc ccc ccg ttc cac ggc acg 304  
 Val Pro Ala Arg Ile Arg Asp Thr Phe Phe Pro Arg Phe His Gly Thr  
 60 65 70  
 cga ctc ctc ccc acc gag gcg cag ccc ggg gag ccg cat ccg tac ctc 352  
 Arg Leu Leu Pro Thr Glu Ala Gln Pro Gly Glu Pro His Pro Tyr Leu  
 75 80 85  
 gtc ctc gac gac ctc ctc gcg ggg ttt gag gcg ccc tgc gtc gca gac 400  
 Val Leu Asp Asp Leu Leu Ala Gly Phe Glu Ala Pro Cys Val Ala Asp  
 90 95 100  
 atc aag atc ggt gcc atc acg tga ccatgagcga tctgctcgga ttccacgtct 454  
 Ile Lys Ile Gly Ala Ile Thr \*  
 105 110  
 ccggcgctcg agtcgtcgcc ccgcaggcgc ccgtgtggcg gacggagcgc cctgagggtga 514  
 aggcctatgga cattgtcggc gtccgcgcgcg tgctccggcg ctgcattgca tccgcttgcc 574  
 ggcgaggggga tggactgcgc gctcgcgcgcg gcggtgtacg gaggaagagg tggagctctg 634  
 tcacagctgc gcgagctcaa ggcgtgggttc gaggggcaga ctctgttcca cttctactcg 694  
 gcgtcgattc ttctgggcta tgatgctgct cagctgcgag caggcggagg tgggggtggg 754  
 gtaacagtga agctgttgga ccttgcccat gtggccgagg gtgatggggt gattgaccac 814  
 aaacttctcg gcgggctctg ctgactgata aagtttgggt ctgacattgt tccagagact 874  
 ccttagacgc agcaaggggc aattc 899

<210> 16  
 <211> 111  
 <212> PRT  
 <213> Zea mays

<400> 16  
 Met Pro Asp Leu His Pro Pro Glu His Gln Val Ala Gly His Arg Ala  
 1 5 10 15  
 Ser Ala Ser Lys Leu Gly Pro Leu Ile Asp Gly Ser Gly Leu Phe Tyr



<210> 19  
 <211> 353  
 <212> DNA  
 <213> Zea mays

<220>  
 <221> misc\_feature  
 <222> (1)...(353)  
 <223> n = A, T, C, or G

<400> 19  
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 ggctatgatg ctgctgcagt cgcancaggc ggaggtgggg gtggggtaac agtgaagctg 120  
 gtggactttg cccatgtggc cgaggggtgat ggggttgatt tgaccacaac ttctggggcg 180  
 agctctgcta gctgatcaag ttccgtttct tgacattggt ccaganactc cttagacgcc 240  
 agcctttggg tccttcctta aaaaaagatc cctgacnttt ttgatttgat tacnaaggaa 300  
 acactttcca ctgtccnaaa aaaaaagccc ntgaggatta aaaaattaac ntt 353

<210> 20  
 <211> 3416  
 <212> DNA  
 <213> Zea mays

<220>  
 <221> CDS  
 <222> (72)...(407)

<400> 20  
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 gtccccatac c atg ccc gac ctc cac ccg ccg gag cac caa gtc gcc ggt 110  
 Met Pro Asp Leu His Pro Pro Glu His Gln Val Ala Gly  
 1 5 10

cac cgc gcc tcc gcc agc aag ctg ggc cca ctc atc gac gac tct ggc 158  
 His Arg Ala Ser Ala Ser Lys Leu Gly Pro Leu Ile Asp Asp Ser Gly  
 15 20 25

ctc ttc tac aag ccg ctc cag gcc ggc gac cgt ggg gag cac gag gtc 206  
 Leu Phe Tyr Lys Pro Leu Gln Ala Gly Asp Arg Gly Glu His Glu Val  
 30 35 40 45

gcc ttc tat gag gcg ttc tcc gcc cac gcc gcc gtc ccg gcc cgc atc 254  
 Ala Phe Tyr Glu Ala Phe Ser Ala His Ala Val Pro Ala Arg Ile  
 50 55 60

cga gac acc ttc ttc ccc cgg ttc cac gcc acg cga ctc ctc ccc acc 302  
 Arg Asp Thr Phe Phe Pro Arg Phe His Gly Thr Arg Leu Leu Pro Thr  
 65 70 75

gag gcg cag ccc ggg gag ccg cat ccg cac ctc gtc ctc gac gac ctc 350  
 Glu Ala Gln Pro Gly Glu Pro His Pro His Leu Val Leu Asp Asp Leu  
 80 85 90

ctc gcg ggg ttt gag gcg ccc tgc gtc gca gac atc aag atc ggt gcc 398  
 Leu Ala Gly Phe Glu Ala Pro Cys Val Ala Asp Ile Lys Ile Gly Ala

atc acg tga ccacgagcgt tctgctcgga ttccgcgctct ccggcgctccg  
 Ile Thr \*  
 110

447

agtcgtcggc cccgagggcg ccgtgtggcg gacggagcgc ccggagggtga aggcctatgga 507  
 catgtgtccg gctccgcggc tgcctccggc ctacgtgtca tccgcttgcc gacgagggga 567  
 tggagctcgc gctcgcggcg gcggtgtacg gaggaaaaagg tggagtcttg tcacagctgc 627  
 gcgactccaa ggcgtgtgtt gaggggcaga ctctgttcca ctctactcgc gcgtcgattc 687  
 ttctgggcta tgaatgctgt gcagtcgcag caggcggagg tgggggtggg gtaacagtga 747  
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 gcgggctctg cttagctgac aagtttgttt ctgacattgt tccagagact cctcagacgc 867  
 agcctttggg tctctcttaa gagaggatcc tggcattttc gatttgataa caaagggaagc 927  
 actttcagct gcaaaaaaag aaagcagcag tgaggatgaa gatgacagta gtgaggaaag 987  
 ttcggatgat gagccaacaa aagttgaaga aaagaaggct ccaaaaagtat cagaaaaat 1047  
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 atgcccata ttaacacctc aggcgatgcca tcatttttgt ttcaacaactc aaaagtaaa 1167  
 gaaaaacatga aaagtatgca ggcagtatga gggacacaca tagttttactg aaactccctt 1227  
 acacagacac atacacaccg tgttctactga aacattcaga ttctactaaa ctgcaacttc 1287  
 tccaaacaaa cactattctg ggcctcggtca agtaacgagc ctccgctcggc ctcgctcttc 1347  
 tagcagcctc aaaaagtcgg ctccggttcgg cgagccaaag agcctgacca taagcatgaa 1407  
 atcagctctcc aaaaataatc ataaagtctc aaaaataatt taagtgcacc gtcttaattt 1467  
 agtaaaaaaa atatatatca tataatatag aaaaataagt aattttgtac agtaaatcaa 1527  
 aaaaataaaa ttaattcatct atttagtacc tataatatat gttaattaaa atttatata 1587  
 caaaaatgtt gttgttttgg ccagctcgcg agctgaactg ctgcgctctg ctgcgctctt 1647  
 ttattgagcc agaaaaaact ctgctcgagc ttgttctaa cagcattttc ggatcgagg 1707  
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 cgcgcctctc ccgtcgccgg gagatggcag caccagcagc tccgcgcgct caaatccac 1827  
 gagtaccagg gcgcggaggt gatgggtaaa tacgggatca acgtgcccg gggcgccgg 1887  
 gctgggtccg tacatgaggt caaggagcgc ttgaagaaca tgttccccg cgagaaagag 1947  
 atagtgttta aaagtcaaat ccttgctggt ggcgcagggc tgggaacttt caaaagcgga 2007  
 ctgcaaggtg gtgtccatct gaggaagctg aatttgattgc aagtaaaatg 2067  
 ttaggccaga ttctgataac gaaacaaact ggtccagagg gaaagattgt gacgaagggtc 2127  
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 aaaaactgct gtccgctcat tattgcttgc agcaagggag gaaaacacta tagttgacct 2247  
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 aatgagatgt tctacttatc ctctcctctg ccatacttac ccactcatggc caatgggggtg 2667  
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 ggagccaaac aagtttatgt ttttatgcga cttcaagagt tgacaaaggt ttaagttctg 2907  
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 aagggaacta tgtgactcat ctgttctggt gatttgatatt ataagtgaata tattctgtga 3087  
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 cgtgtatgga gacagggaca agccagcgct tataatgttt acagagatgt ggttctgtga 3207  
 ctggtgcgct gtactcaggg tttatttcaa caagatttaa atatgagatg tagagtgtt 3267  
 gatgtacatc acttctacta tcatgaaatc tgtagaagcg gaaactacta gccatatatg 3327  
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 tgaattatca aaaaaaaaaa aaaaaaaaaa 3416

<210> 21  
 <211> 111  
 <212> PRT  
 <213> Zea mays

<400> 21  
 Met Pro Asp Leu His Pro Pro Glu His Gln Val Ala Gly His Arg Ala  
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 Ser Ala Ser Lys Leu Gly Pro Leu Ile Asp Asp Ser Gly Leu Phe Tyr  
 20 25 30  
 Lys Pro Leu Gln Ala Gly Asp Arg Gly Glu His Glu Val Ala Phe Tyr  
 35 40 45  
 Glu Ala Phe Ser Ala His Ala Val Pro Ala Arg Ile Arg Asp Thr  
 50 55 60  
 Phe Phe Pro Arg Phe His Gly Thr Arg Leu Leu Pro Thr Glu Ala Gln  
 65 70 75 80  
 Pro Gly Glu Pro His Pro His Leu Val Leu Asp Asp Leu Leu Ala Gly  
 85 90 95  
 Phe Glu Ala Pro Cys Val Ala Asp Ile Lys Ile Gly Ala Ile Thr  
 100 105 110

<210> 22  
 <211> 1448  
 <212> DNA  
 <213> Parthenium argentatum

<220>  
 <221> CDS  
 <222> (52)...(1020)

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 cca gct cca gct gtt cct aat ggc acg ggt gct cgc ctt aag gac gaa 105  
 Pro Ala Pro Ala Val Pro Asn Gly Thr Gly Ala Pro Leu Lys Asp Glu  
 5 10 15  
 cct tcc aac ccc gat cag gcg cag cac cag cct gac gag cgc gtt caa 153  
 Pro Ser Asn Pro Asp Gln Ala Gln His Gln Pro Asp Glu Arg Val Gln  
 20 25 30  
 cac ttc atc ctt ctt gaa gac ctt act gct ggc atg aca agg cct tgt 201  
 His Phe Ile Leu Leu Glu Asp Leu Thr Ala Gly Met Thr Arg Pro Cys  
 35 40 45 50  
 gtc tta gac ttg aag atg ggt acg cgc cag tat ggt gtg gaa gcc gat 249  
 Val Leu Asp Leu Lys Met Gly Thr Arg Gln Tyr Gly Val Glu Ala Asp  
 55 60 65  
 gag aag aaa cag cgg tct caa cgg cgc aag tgt cag atg acc acc agt 297  
 Glu Lys Lys Gln Arg Ser Gln Arg Lys Cys Gln Met Thr Thr Ser  
 70 75 80

gct caa ctc ggc gtg cga gtc tgc ggt atg caa att tgg aac gcc aag	345
Ala Gln Leu Gly Val Arg Val Cys Gly Met Gln Ile Trp Asn Ala Lys	
85 90 95	
acc cag agc tac atc ttc gag gac aag tac ttc ggt cga gat ctg aaa	393
Thr Gln Ser Tyr Ile Phe Glu Asp Lys Tyr Phe Gly Arg Asp Leu Lys	
100 105 110	
gca gga aaa gaa ttt cag gac gcg ctt aag cgc ttt ttt tgg gat ggg	441
Ala Gly Lys Glu Phe Gln Asp Ala Leu Lys Arg Phe Phe Trp Asp Gly	
115 120 125 130	
acg agc tac aaa gca gca aac aga cac ata ccc gtc ata ttg gag aag	489
Thr Ser Tyr Lys Ala Ala Asn Arg His Ile Pro Val Ile Leu Glu Lys	
135 140 145	
atc agc caa ctg gaa cgc atg ata cga aaa ctt cca gga tac aga ttc	537
Ile Ser Gln Leu Glu Arg Met Ile Arg Lys Leu Pro Gly Tyr Arg Phe	
150 155 160	
tac gcg agt agt ttg ttg atg ctc tat gat cgt ggg gac ggt gag tcg	585
Tyr Ala Ser Ser Leu Leu Met Leu Tyr Asp Arg Gly Asp Gly Glu Ser	
165 170 175	
aag gag aaa gac gca gca ccc tct tta cct aac ggc ttg tcg aac ccg	633
Lys Glu Lys Asp Ala Ala Pro Ser Leu Pro Asn Gly Leu Ser Asn Pro	
180 185 190	
agc aac gaa gac gtt tca aca ata cca tct gga ctt aca tca cca ggg	681
Ser Asn Glu Asp Val Ser Thr Ile Pro Ser Gly Leu Thr Ser Pro Gly	
195 200 205 210	
ccg aca gtc gct tct aaa ccg tca ccc aag aag cac gga gag atc aag	729
Pro Thr Val Ala Ser Lys Pro Ser Pro Lys Lys His Gly Glu Ile Lys	
215 220 225	
ctg aaa att gtc gac ttt gcc aac tgc gtg act gca gaa gac cct cta	777
Leu Lys Ile Val Asp Phe Ala Asn Cys Val Thr Ala Glu Asp Pro Leu	
230 235 240	
cca gac gac tta cct tgt cca cct gaa aat ccc gac ggc atc gat aga	825
Pro Asp Asp Leu Pro Cys Pro Pro Glu Asn Pro Asp Gly Ile Asp Arg	
245 250 255	
ggg tac ctc cgt ggc ctc cga tca cta cgc ctc tac ttc caa cgc att	873
Gly Tyr Leu Arg Gly Leu Arg Ser Leu Arg Leu Tyr Phe Gln Arg Ile	
260 265 270	
tgg aat gac atc aac gag gaa tgg gtc gaa cga ggc gag ggc gag ggc	921
Trp Asn Asp Ile Asn Glu Glu Trp Val Glu Arg Gly Glu Gly Glu Gly	
275 280 285 290	
atg gcg cga aat cat cac cat ggc cct ggt tta ggt gag gtt ggt gcg	969
Met Ala Arg Asn His His His Gly Pro Gly Leu Gly Glu Val Gly Ala	
295 300 305	

ggc tgg atg gat gat gct ggt ggt gag gat aca ggc tac gcc agt ttc 1017  
 Gly Trp Met Asp Asp Ala Gly Gly Glu Asp Thr Gly Tyr Ala Ser Phe  
 310 315 320

taa agaagaggag gaacagcaaa gctgcccacg ctcgacagaa gtcggacagt 1070

cgatattgat acgtccatcc cttttccctt cccttcattt ccacgttcag tctatttcac 1130  
 attgtgtgca tttttgggtg caagcatggt gttttggtgc ataattgtaa gacaaagggt 1190  
 aatgaaattg gcaactcttt tggcatgcat cggcgacagca ttttatgggc ggtcagaacc 1250  
 tctgcgttgt ggcttttagt ttttgaattt tgcggaatct ggggtgttct tgaggcggat 1310  
 tctttgtata ttatcataaa gagtagggta gcgctagctc attaatacaa cactttgaat 1370  
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<210> 23

<211> 322

<212> PRT

<213> Parthenium argentatum

<400> 23

Met Leu Pro Ala Pro Ala Val Pro Asn Gly Thr Gly Ala Pro Leu Lys  
 1 5 10 15  
 Asp Glu Pro Ser Asn Pro Asp Gln Ala Gln His Gln Pro Asp Glu Arg  
 20 25 30  
 Val Gln His Phe Ile Leu Leu Glu Asp Leu Thr Ala Gly Met Thr Arg  
 35 40 45  
 Pro Cys Val Leu Asp Leu Lys Met Gly Thr Arg Gln Tyr Gly Val Glu  
 50 55 60  
 Ala Asp Glu Lys Lys Gln Arg Ser Gln Arg Arg Lys Cys Gln Met Thr  
 65 70 75 80  
 Thr Ser Ala Gln Leu Gly Val Arg Val Cys Gly Met Gln Ile Trp Asn  
 85 90 95  
 Ala Lys Thr Gln Ser Tyr Ile Phe Glu Asp Lys Tyr Phe Gly Arg Asp  
 100 105 110  
 Leu Lys Ala Gly Lys Glu Phe Gln Asp Ala Leu Lys Arg Phe Phe Trp  
 115 120 125  
 Asp Gly Thr Ser Tyr Lys Ala Ala Asn Arg His Ile Pro Val Ile Leu  
 130 135 140  
 Glu Lys Ile Ser Gln Leu Glu Arg Met Ile Arg Lys Leu Pro Gly Tyr  
 145 150 155 160  
 Arg Phe Tyr Ala Ser Ser Leu Leu Met Leu Tyr Asp Arg Gly Asp Gly  
 165 170 175  
 Glu Ser Lys Glu Lys Asp Ala Ala Pro Ser Leu Pro Asn Gly Leu Ser  
 180 185 190  
 Asn Pro Ser Asn Glu Asp Val Ser Thr Ile Pro Ser Gly Leu Thr Ser  
 195 200 205  
 Pro Gly Pro Thr Val Ala Ser Lys Pro Ser Pro Lys Lys His Gly Glu  
 210 215 220  
 Ile Lys Leu Lys Ile Val Asp Phe Ala Asn Cys Val Thr Ala Glu Asp  
 225 230 235 240  
 Pro Leu Pro Asp Asp Leu Pro Cys Pro Pro Glu Asn Pro Asp Gly Ile  
 245 250 255  
 Asp Arg Gly Tyr Leu Arg Gly Leu Arg Ser Leu Arg Leu Tyr Phe Gln  
 260 265 270



Arg Ile Trp Asn Asp Ile Asn Glu Glu Trp Val Glu Arg Gly Glu Gly  
 275 280 285  
 Glu Gly Met Ala Arg Asn His His Gly Pro Gly Leu Gly Glu Val  
 290 295 300  
 Gly Ala Gly Trp Met Asp Asp Ala Gly Gly Glu Asp Thr Gly Tyr Ala  
 305 310 315 320  
 Ser Phe

<210> 24  
 <211> 2270  
 <212> DNA  
 <213> Zea mays

<220>  
 <221> CDS  
 <222> (3)...(953)

<400> 24  
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 Thr Arg Pro Arg Lys Leu Arg Asn Ile Val Gln Trp Thr Pro Phe  
 1 5 10 15  
 ttt caa act tac aaa aaa cag agg tat cca tgg gta cag cta gcc gga 95  
 Phe Gln Thr Tyr Lys Lys Gln Arg Tyr Pro Trp Val Gln Leu Ala Gly  
 20 25 30  
 cac caa ggc aat ttc aaa gcc ggt ccg gaa cct ggt acg atc ctc aag 143  
 His Gln Gly Asn Phe Lys Ala Gly Pro Gly Thr Ile Leu Lys  
 35 40 45  
 aaa ctt tgt ccc aaa gaa cag ttg tgc ttc caa gtg ctg atg aag gac 191  
 Lys Leu Cys Pro Lys Glu Gln Leu Cys Phe Gln Val Leu Met Lys Asp  
 50 55 60  
 gtt ctg aga ccg tac gtg ccc gaa tac aag ggc cac ttg act acc gac 239  
 Val Leu Arg Pro Tyr Val Pro Glu Tyr Lys Gly His Leu Thr Thr Asp  
 65 70 75  
 gac gga gac cta tat ctt cag cta gaa gac ttg ttg ggt gac ttc act 287  
 Asp Gly Asp Leu Tyr Leu Gln Leu Glu Asp Leu Leu Gly Asp Phe Thr  
 80 85 90 95  
 tcg ccg tgc gtc atg gac tgc aag atc ggc gtc agg acg tat ctg gaa 335  
 Ser Pro Cys Val Met Asp Cys Lys Ile Gly Val Arg Thr Tyr Leu Glu  
 100 105 110  
 gag gaa ctg gcg aaa gcc aaa gag aaa ccc, aag ttg aga aaa gac atg 383  
 Glu Glu Leu Ala Lys Ala Lys Glu Lys Pro Lys Leu Arg Lys Asp Met  
 115 120 125  
 tac gaa aaa atg att cag ata gac ccc aac gca cca tcg gag gag gaa 431  
 Tyr Glu Lys Met Ile Gln Ile Asp Pro Asn Ala Pro Ser Glu Glu Glu  
 130 135 140

cac cga ctg aag ggt gtg aca aaa ccg agg tac atg gtt tgg agg gag	479
His Arg Leu Lys Gly Val Thr Lys Pro Arg Tyr Met Val Trp Arg Glu	
145 150 155	
acg att tcg tcc acg gcc acg ttg ggc ttc cgg atc gag ggg atc aag	527
Thr Ile Ser Ser Thr Ala Thr Leu Gly Phe Arg Ile Glu Gly Ile Lys	
160 165 170 175	
aaa agc gat gga aaa tcg agc aag gac ttc aag acg aca aag aac cgg	575
Lys Ser Asp Gly Lys Ser Ser Lys Asp Phe Lys Thr Thr Lys Asn Arg	
180 185 190	
gac cag gtg atc gaa gcg ttt cga gat ttc gtc gcc ggt ttc ccg cac	623
Asp Gln Val Ile Glu Ala Phe Arg Asp Phe Val Ala Gly Phe Pro His	
195 200 205	
gta atc ccc aag tac ata aac cga ctg aga gcg atc aga gac ata ctg	671
Val Ile Pro Lys Tyr Ile Asn Arg Leu Arg Ala Ile Arg Asp Ile Leu	
210 215 220	
gtg aac tcc aag ttt ttc act acg cac gag gtg atc ggc agc tcg ctg	719
Val Asn Ser Lys Phe Phe Thr Thr His Glu Val Ile Gly Ser Ser Leu	
225 230 235	
ctg ttc gtg cac gac agc aag aac gcc aac ata tgg ctt atc gac ttc	767
Leu Phe Val His Asp Ser Lys Asn Ala Asn Ile Trp Leu Ile Asp Phe	
240 245 250 255	
gca aag acg ctc ata ctt ccg ccg gac atc cgg atc aac cac acg tcc	815
Ala Lys Thr Leu Ile Leu Pro Pro Asp Ile Arg Ile Asn His Thr Ser	
260 265 270	
gag tgg gtg gtg ggc aac cac gag gac ggt tac ctg atc ggt atc aac	863
Glu Trp Val Val Gly Asn His Glu Asp Gly Tyr Leu Ile Gly Ile Asn	
275 280 285	
aac ctg ctg gac ata ttc acc gat atg aac gcc gcc acc gcg ttt ccc	911
Asn Leu Leu Asp Ile Phe Thr Asp Met Asn Ala Ala Thr Ala Phe Pro	
290 295 300	
gtc acg ctc atc gaa gtc acg gcc ccg tcc gaa gtc acc tga	953
Val Thr Leu Ile Glu Val Thr Ala Pro Ser Glu Val Thr *	
305 310 315	
acgcgcgtcga tcccgcgcgg tacccctgact cgctcggcga cccactcgcc ggtgtcattc	1013
gattccagcc acccactcag tggctcttgcg aatccagtgga cccaccccggt tgacaatgtg	1073
tgataataat aatatgtctcg gcgcacaaata ttccaaaag tcttttttaa attacacttt	1133
cgattttcga cgcacaaaca aatgacgacg ttttccgtac ctacctactg taggggttcg	1193
tccgatttga atcataattt attttacccc caccacaacc cccaaccggt tatggcccac	1253
cagaggattt gccatcagta ttaaaacaat gatctattat agatgtttaa aaataaatat	1313
tatataatta tacatcatcg cgggtgtgttg tgtaatatgc ctattataat atgtactata	1373
ttatacacat agcatattat aaaaatagta tattattata ttattattata ataataattat	1433
ggttatgtgt gtttgtgtgg aaatccaata atataaaata atagttatta tttttaaata	1493
ctgtgacgat aatgggacta ctacgtgtga ttctcaaatg atatatatat attaatattt	1553
taaacgtaca tttttaattc caaacgtata tgacgtgtgt atatatatat atgatataat	1613
aattactata ctgtgcgtgc gataacataa taatttttga cctaatacat caatcaatta	1673

tccactgcag tgcgtgtgg tttttatttc gttgttttat tttatcgcta tcactaaaatt 1733  
 actatttttta ttattatttat tttttttttt ttccaaaaac tttgttttat aatcagctcc 1793  
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 ttatttcctc acgaaaaaga gaagtcctca tttctttctc ccgttacagt gtgtgtgtgt 1973  
 gtgtgtgtgt gtgtgtgtgt gtgtgtgtgt gcgtatgtgt atgtgtgaaa tttttgattt 2033  
 aattatataat tattataatt ttttctcctt atatttttat ttattattat aacatttttt 2093  
 ttgtgtgtac agaattattta aataagactt gtaaaagaaa cccttggttat attattttat 2153  
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<210> 25  
 <211> 316  
 <212> PRT  
 <213> Zea mays

<400> 25  
 Thr Arg Pro Arg Lys Leu Arg Asn Ile Val Gln Trp Thr Pro Phe Phe  
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 Gln Thr Tyr Lys Lys Gln Arg Tyr Pro Trp Val Gln Leu Ala Gly His  
 20 25 30  
 Gln Gly Asn Phe Lys Ala Gly Pro Glu Pro Gly Thr Ile Leu Lys Lys  
 35 40 45  
 Leu Cys Pro Lys Glu Gln Leu Cys Phe Gln Val Leu Met Lys Asp Val  
 50 55 60  
 Leu Arg Pro Tyr Val Pro Glu Tyr Lys Gly His Leu Thr Thr Asp Asp  
 65 70 75 80  
 Gly Asp Leu Tyr Leu Gln Leu Glu Asp Leu Leu Gly Asp Phe Thr Ser  
 85 90 95  
 Pro Cys Val Met Asp Cys Lys Ile Gly Val Arg Thr Tyr Leu Glu Glu  
 100 105 110  
 Glu Leu Ala Lys Ala Lys Glu Lys Pro Lys Leu Arg Lys Asp Met Tyr  
 115 120 125  
 Glu Lys Met Ile Gln Ile Asp Pro Asn Ala Pro Ser Glu Glu Glu His  
 130 135 140  
 Arg Leu Lys Gly Val Thr Lys Pro Arg Tyr Met Val Trp Arg Glu Thr  
 145 150 155 160  
 Ile Ser Ser Thr Ala Thr Leu Gly Phe Arg Ile Glu Gly Ile Lys Lys  
 165 170 175  
 Ser Asp Gly Lys Ser Ser Lys Asp Phe Lys Thr Thr Lys Asn Arg Asp  
 180 185 190  
 Gln Val Ile Glu Ala Phe Arg Asp Phe Val Ala Gly Phe Pro His Val  
 195 200 205  
 Ile Pro Lys Tyr Ile Asn Arg Leu Arg Ala Ile Arg Asp Ile Leu Val  
 210 215 220  
 Asn Ser Lys Phe Phe Thr Thr His Glu Val Ile Gly Ser Ser Leu Leu  
 225 230 235 240  
 Phe Val His Asp Ser Lys Asn Ala Asn Ile Trp Leu Ile Asp Phe Ala  
 245 250 255  
 Lys Thr Leu Ile Leu Pro Pro Asp Ile Arg Ile Asn His Thr Ser Glu  
 260 265 270  
 Trp Val Val Gly Asn His Glu Asp Gly Tyr Leu Ile Gly Ile Asn Asn  
 275 280 285  
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 Thr Leu Ile Glu Val Thr Ala Pro Ser Glu Val Thr

305

310

315

<210> 26  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Primer

<400> 26  
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25

<210> 27  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Primer

<400> 27  
 ccttagacgc agcctttggg tccttcttaa

30

<210> 28  
 <211> 36  
 <212> DNA  
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<220>  
 <223> Primer

<400> 28  
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36

<210> 29  
 <211> 21  
 <212> PRT  
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<220>  
 <223> Consensus Sequence

<400> 29  
 Ile Leu Leu Glu Asn Leu Thr Ser Arg Tyr Glu Val Pro Cys Val Leu  
 1 5 10 15  
 Asp Leu Lys Met Gly  
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<210> 30  
 <211> 33  
 <212> PRT  
 <213> Artificial Sequence

<220>

<223> Consensus Sequence

<221> VARIANT

<222> (1)...(33)

<223> Xaa = any amino acid

<400> 30

Leu Lys Xaa Pro Glu His Gln Val Ala Gly His Xaa Ala Xaa Xaa Gly  
1 5 10 15  
Lys Xaa Gly Pro Leu Val Asp Asp Xaa Gly Xaa Phe Tyr Lys Pro Leu  
20 25 30  
Gln

<210> 31

<211> 33

<212> PRT

<213> Artificial Sequence

<220>

<223> Consensus Sequence

<221> VARIANT

<222> (1)...(33)

<223> Xaa = any amino acid

<400> 31

Leu Lys Xaa Pro Glu His Gln Val Ala Gly His Xaa Ala Xaa Xaa Gly  
1 5 10 15  
Lys Xaa Gly Pro Leu Ile Asp Asp Xaa Gly Xaa Phe Tyr Lys Pro Leu  
20 25 30  
Gln

<210> 32

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<213> Artificial Sequence

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<223> Xaa = any amino acid

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Leu Lys Xaa Pro Asp His Gln Val Ala Gly His Xaa Ala Xaa Xaa Gly  
1 5 10 15  
Lys Xaa Gly Pro Leu Val Asp Asp Xaa Gly Xaa Phe Tyr Lys Pro Leu  
20 25 30  
Gln

<210> 33  
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<400> 33  
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 Lys Xaa Gly Pro Leu Ile Asp Asp Xaa Gly Xaa Phe Tyr Lys Pro Leu  
 20 25 30  
 Gln

<210> 34  
 <211> 41  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Consensus Sequence

<221> VARIANT  
 <222> (1)...(41)  
 <223> Xaa = any amino acid

<400> 34  
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 1 5 10 15  
 Val Lys Xaa Gly Ser Arg Thr Trp Xaa Xaa Xaa Xaa Xaa Glu Xaa Tyr  
 20 25 30  
 Ile Xaa Lys Cys Leu Xaa Lys Asp Arg  
 35 40

<210> 35  
 <211> 41  
 <212> PRT  
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<221> VARIANT  
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 <223> Xaa = any amino acid

<400> 35

Val Leu Xaa Asp Leu Xaa Xaa Xaa Xaa Xaa Pro Ser Val Met Asp  
1 5 10 15  
Ile Lys Xaa Gly Ser Arg Thr Trp Xaa Xaa Xaa Xaa Glu Xaa Tyr  
20 25 30  
Ile Xaa Lys Cys Leu Xaa Lys Asp Arg  
35 40

<210> 36

<211> 41

<212> PRT

<213> Artificial Sequence

<220>

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<221> VARIANT

<222> (1)...(41)

<223> Xaa = any amino acid

<400> 36

Val Leu Xaa Asp Leu Xaa Xaa Xaa Xaa Xaa Pro Cys Val Met Asp  
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Val Lys Xaa Gly Ser Arg Thr Trp Xaa Xaa Xaa Xaa Glu Xaa Tyr  
20 25 30  
Ile Xaa Lys Cys Leu Xaa Lys Asp Arg  
35 40

<210> 37

<211> 41

<212> PRT

<213> Artificial Sequence

<220>

<223> Consensus Sequence

<221> VARIANT

<222> (1)...(41)

<223> Xaa = any amino acid

<400> 37

Val Leu Xaa Asp Leu Xaa Xaa Xaa Xaa Xaa Pro Cys Val Met Asp  
1 5 10 15  
Ile Lys Xaa Gly Ser Arg Thr Trp Xaa Xaa Xaa Xaa Glu Xaa Tyr  
20 25 30  
Ile Xaa Lys Cys Leu Xaa Lys Asp Arg  
35 40